

## FIGURE 1

GCTCCCAAGCAAGAACCTCGGGGCGGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA  
CAAGAAGCCGCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCGCGCGCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCTGGAAGTGCAGCGGGGGC  
CAGAGCGCGCACAGTTTGTGAGAGATCAAGGCAGTGGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGGGTACCTCTGCATGGGGCGCCGACGGCAAGATGCAGGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGGCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTACCCGACTGGAGGCGGTGAGGAGTCCAGCTTTGAGAAG**TAA**CT  
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGGCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGC  
TTCCATCTCCAGCCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGTGTGT

## **FIGURE 2**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVFYLCMGADGKMQLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

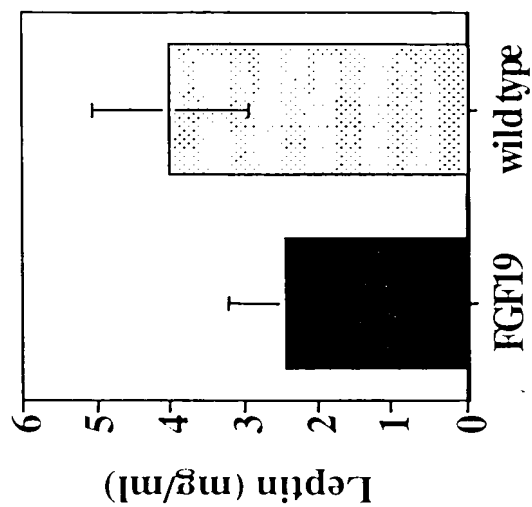
**signal peptide:**  
amino acids 1-22

**N-myristoylation sites:**  
amino acids 15-21, 54-60, 66-72, 201-207

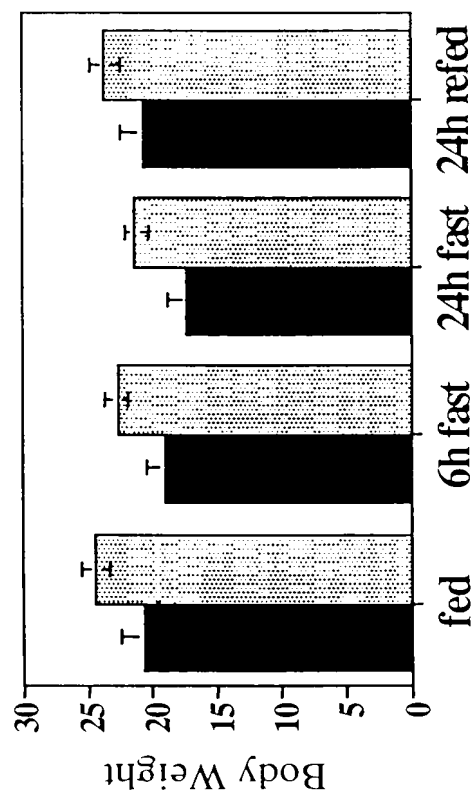
**Prokaryotic membrane lipoprotein lipid attachment site:**  
amino acids 48-59

**HBGF/FGF domain:**  
amino acids 80-131

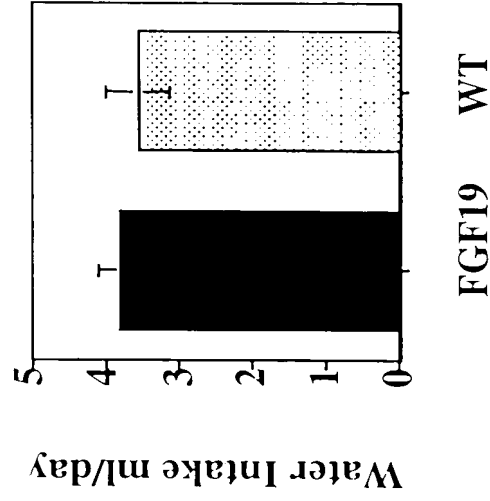
**FIGURE 3B**



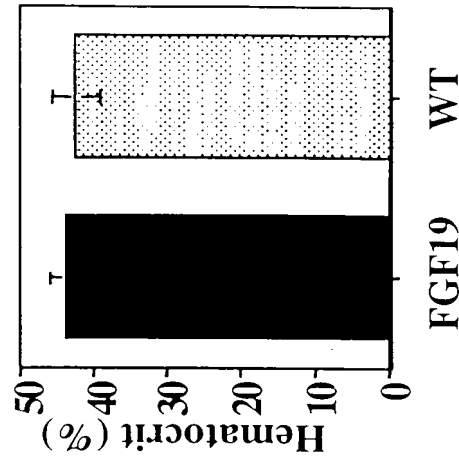
**FIGURE 3A**



**FIGURE 4B**



**FIGURE 4D**



**FIGURE 4C**

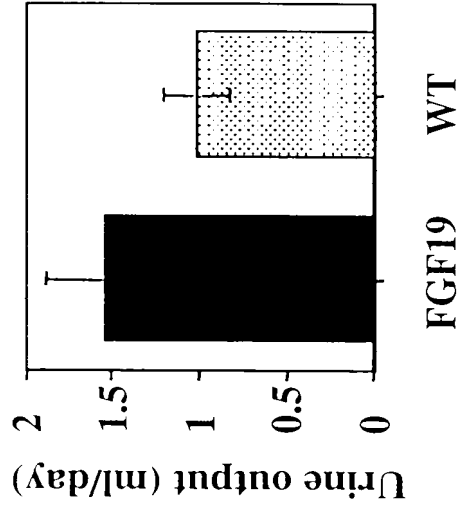
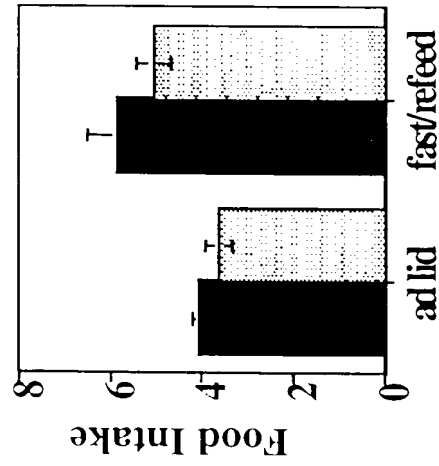


FIGURE 5

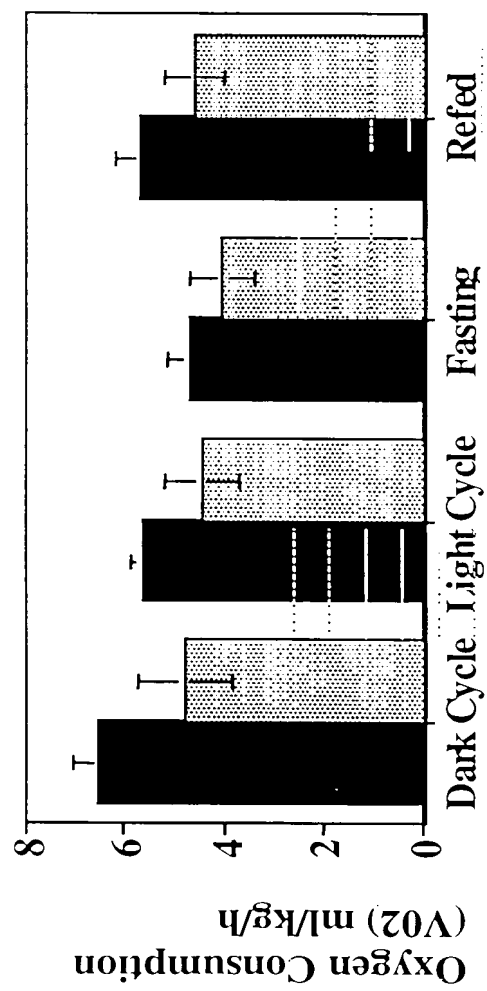


FIGURE 6B

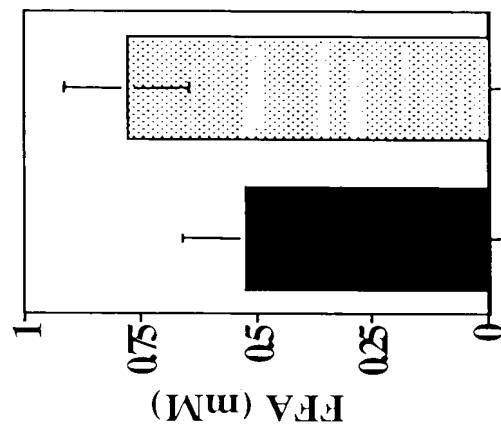


FIGURE 6A

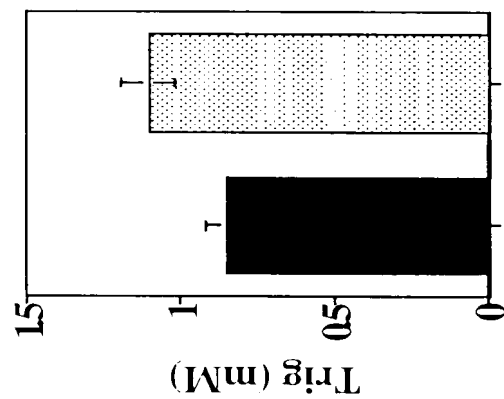


FIGURE 7B

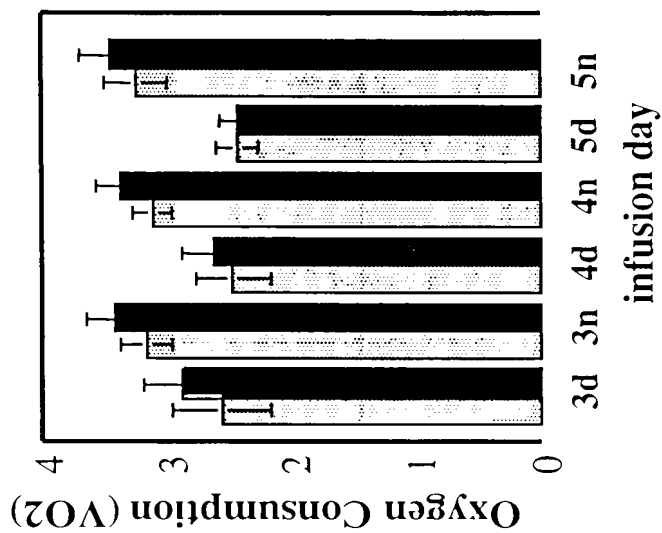
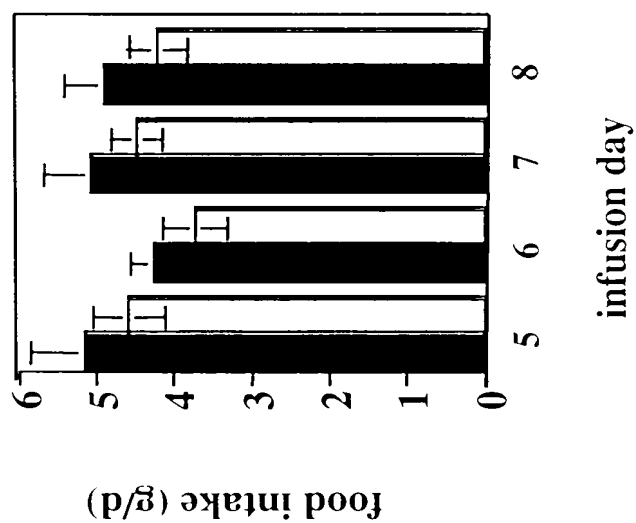
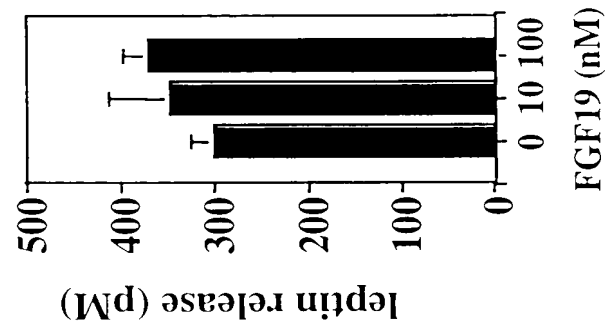


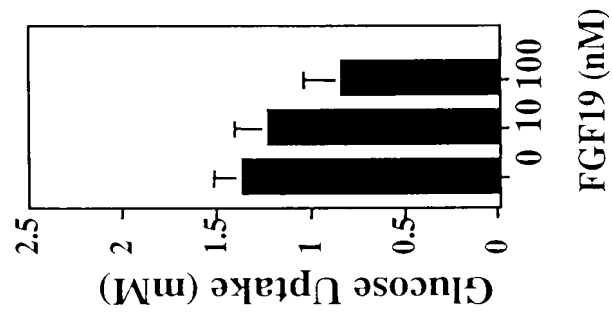
FIGURE 7A



**FIGURE 8A**



**FIGURE 8B**





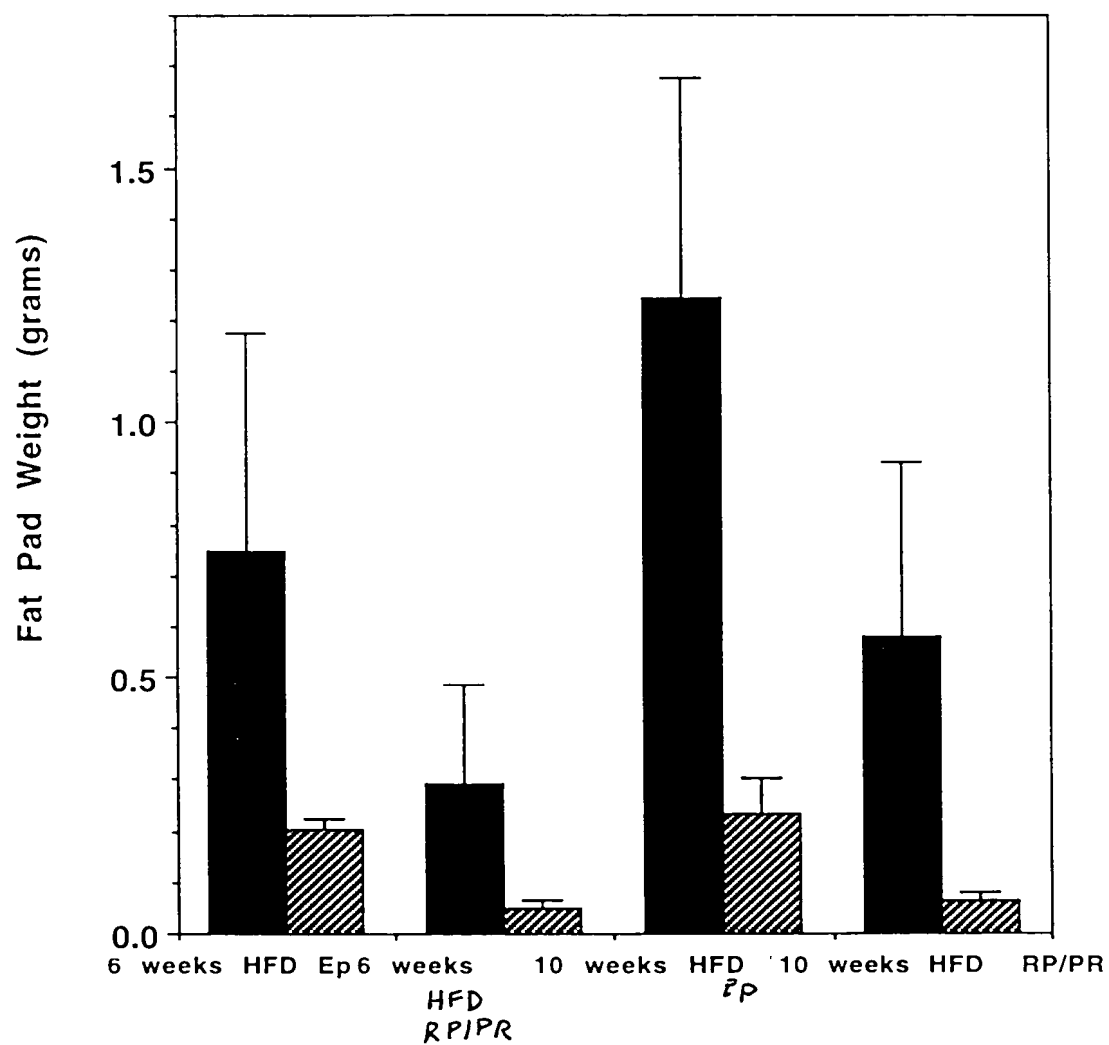
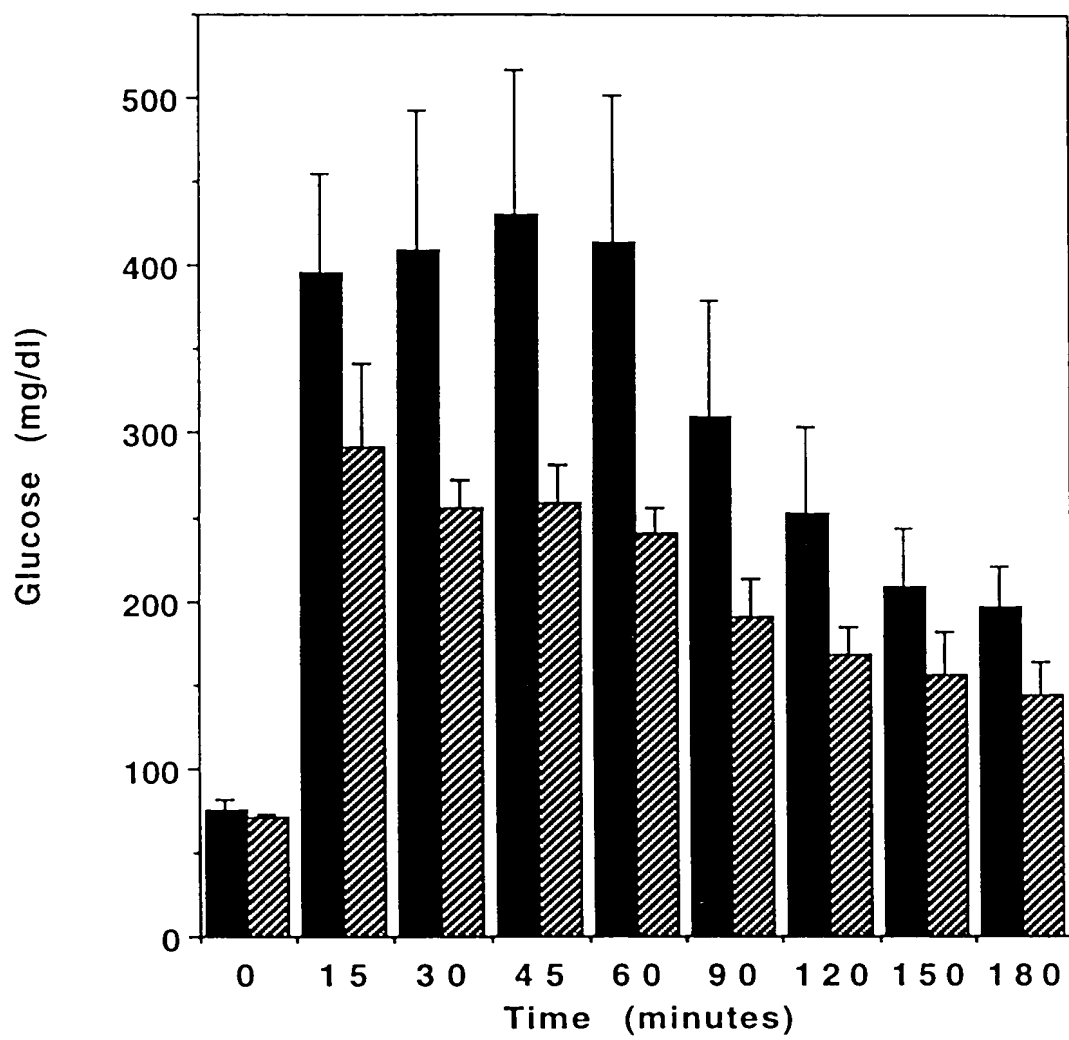


FIGURE 9



**FIGURE 10**